

Supplementary Materials

Supplementary Tables

Table S1 The detailed search strategies of the associations between GC (rs4588, rs7041), CYP27B1 (rs4646537, and rs3782130) polymorphisms and cancer risk

Database	Search strategy
Pubmed	#1: Polymorphism, genetic #2: Polymorphism* #3: SNP #4: Single nucleotide polymorphism #5: Variant #6: Mutation #7: #1 OR #2 OR #3 OR #4 OR #5 OR #6 #8: rs4588 #9: rs7041 #10: rs4646537 #11: rs3782130 #12: vitamin D-binding protein #13: CYP27B1 #14: #8 OR #9 OR #10 OR #11 OR #12 OR #13 #15: Neoplasms #16: Cancer #17: Carcino* #18: #15 OR #16 OR #17 #19: #7 AND #14 AND #18
Embase	#1: 'neoplasm'/exp OR #2: cancer OR tumor OR #3: tumor carcinoma OR #4: carcinoma carcinogenesis) AND #5: carcinogenesis (rs4588 OR rs7041 OR #6: #1 OR #2 OR #3 OR #4 OR #5 rs4646537 OR rs3782130 #7: rs4588 OR CYP24A1 OR #8: rs7041 vitamin D-binding protein #9: rs4646537 OR CYP27B1) AND #10: rs3782130 ('single nucleotide #11: vitamin D-binding protein polymorphism'/exp OR #12: CYP27B1 SNP OR polymorphism #13: #7 OR #8 OR #9 OR #10 OR #11 OR #12 OR variant OR #14: 'single nucleotide polymorphism'/exp mutation)) #15: SNP

#16: polymorphism

#17: variant

#18: mutation

#19: #14 OR #15 OR #16 OR #17 OR #18

#20: #6 AND #13 AND #19

Table S2. Score of quality assessment

Criteria	Score
Representativeness of case	
Selected from population cancer registry	2
Selected from hospital	1
No method of selection described	0
Representativeness of control	
Population-based	3
Blood donors	2
Hospital-based	1
Not described	0
Ascertainment of cancer case	
Histopathologic confirmation	2
By patient medical record	1
Not described	0
Control selection	
Controls matched with cases by age and sex	2
Controls matched with cases only by age or by sex	1
Not matched or not described	0
Genotyping examination	
Genotyping done blindly and quality control	2
Only genotyping done blindly or quality control	1
Unblinded and without quality control	0
HWE	
HWE in the control group	1
HWD in the control group or not mentioned	0
Total sample size	
> 1000	3
501 - 1000	2
201 - 500	1
≤ 200	0

Table S3. False-positive report probability values for associations between the rs7041 polymorphism and cancer risk

Significant association	OR (95%CI)	<i>P</i> ^a	Statistical power ^b	Prior probability				
				0.25	0.1	0.01	0.001	0.0001
Dominant								
Overall	1.22(1.03, 1.44)	0.019	0.993	0.054	0.145	0.651	0.950	0.995
PB	1.28(1.04, 1.59)	0.023	0.924	0.077	0.200	0.733	0.965	0.996
Recessive								
Overall	1.27(1.02, 1.58)	0.030	0.932	0.093	0.236	0.772	0.972	0.997
Asian	1.40(1.11, 1.77)	0.005	0.718	0.020	0.058	0.404	0.873	0.986
Non-small cell lung cancer	1.73(1.05, 2.84)	0.031	0.286	0.240	0.487	0.913	0.991	0.999
PB	1.30(1.01, 1.68)	0.045	0.863	0.135	0.319	0.837	0.981	0.998
PCR-RFLP	1.55(1.10, 2.19)	0.013	0.426	0.084	0.215	0.750	0.968	0.997
Homozygote								
Overall	1.41(1.06, 1.88)	0.017	0.663	0.080	0.207	0.742	0.967	0.997
Asian	1.52(1.19, 1.93)	0.001	0.457	0.004	0.011	0.113	0.563	0.928
Non-small cell lung cancer	1.97(1.38, 2.81)	0.000	0.066	0.008	0.024	0.214	0.734	0.965
PB	1.49(1.05, 2.09)	0.024	0.515	0.108	0.267	0.801	0.976	0.998
PCR-RFLP	1.66(1.03, 2.69)	0.039	0.340	0.259	0.512	0.920	0.991	0.999
Heterozygote								
Asian	1.28(1.00, 1.63)	0.047	0.901	0.131	0.312	0.833	0.980	0.998
PCR-RFLP	1.48(1.09, 2.01)	0.013	0.534	0.063	0.169	0.691	0.958	0.996
Allele								
Overall	1.17(1.02, 1.33)	0.022	1.000	0.047	0.128	0.618	0.942	0.994
Asian	1.20(1.09, 1.32)	0.000	1.000	0.001	0.002	0.017	0.150	0.639
Non-small cell lung cancer	1.32(1.09, 1.60)	0.004	0.904	0.015	0.044	0.339	0.838	0.981

PB	1.20(1.02, 1.42)	0.029	0.995	0.092	0.234	0.771	0.971	0.997
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The results in false-positive report probability analysis were in bold, if the prior probability <0.2 . OR: odds ratio; CI: confidence interval; ^a P value for significant test; ^b Statistical power was calculated using the number of observations in the meta-analysis and the OR and P value in this table.

Table S4. False-positive report probability values for associations between the rs4588 polymorphism and cancer risk

Significant association	OR (95%CI)	<i>P</i> ^a	Statistical power ^b	Prior probability				
				0.25	0.1	0.01	0.001	0.0001
Dominant								
Overall	1.10(1.02, 1.19)	0.016	1.000	0.050	0.136	0.634	0.946	0.994
Caucasian	1.10(1.01, 1.21)	0.040	1.000	0.130	0.310	0.832	0.980	0.998
Breast cancer	1.10(1.00, 1.21)	0.046	1.000	0.130	0.310	0.832	0.980	0.998
PB	1.10(1.00, 1.20)	0.040	1.000	0.087	0.223	0.759	0.969	0.997
High quality (> 9)	1.16(1.02, 1.32)	0.047	1.000	0.068	0.180	0.707	0.961	0.996
Recessive								
Overall	1.27(1.11, 1.46)	0.001	0.990	0.002	0.007	0.072	0.440	0.887
Caucasian	1.17(1.00, 1.39)	0.049	0.998	0.182	0.401	0.880	0.987	0.999
Asian	1.51(1.18, 1.94)	0.001	0.479	0.008	0.023	0.207	0.725	0.964
Digestive system tumor	1.58(1.02, 2.46)	0.042	0.409	0.239	0.485	0.912	0.991	0.999
PB	1.19(1.02, 1.40)	0.029	0.997	0.097	0.245	0.781	0.973	0.997
HB	1.58(1.02, 2.46)	0.042	0.409	0.239	0.485	0.912	0.991	0.999
PCR-RFLP	1.35(1.13, 1.61)	0.001	0.879	0.003	0.009	0.086	0.488	0.905
High quality (> 9)	1.55(1.23, 1.96)	0.000	0.392	0.002	0.006	0.060	0.391	0.865
Homozygote								
Overall	1.31(1.13, 1.51)	0.000	0.969	0.001	0.002	0.020	0.168	0.668
Caucasian	1.22(1.02, 1.45)	0.026	0.990	0.068	0.179	0.706	0.960	0.996
Asian	1.56(1.06, 2.29)	0.024	0.421	0.142	0.331	0.845	0.982	0.998
Breast cancer	1.20(1.00, 1.43)	0.047	0.994	0.111	0.273	0.805	0.977	0.998
PB	1.23(1.05, 1.45)	0.013	0.991	0.040	0.110	0.577	0.932	0.993
PCR-RFLP	1.45(1.08, 1.94)	0.014	0.590	0.059	0.159	0.675	0.954	0.995

High quality (> 9)	1.59(1.25, 2.04)	0.000	0.323	0.002	0.007	0.075	0.450	0.891
Heterozygote								
Overall	1.23(1.06, 1.42)	0.005	0.997	0.014	0.041	0.320	0.826	0.979
Asian	1.51(1.16, 1.96)	0.002	0.480	0.012	0.035	0.287	0.803	0.976
Digestive system tumor	1.54(1.15, 2.08)	0.004	0.432	0.033	0.092	0.528	0.918	0.991
PCR-RFLP	1.34(1.12, 1.62)	0.002	0.878	0.008	0.025	0.220	0.740	0.966
High quality (> 9)	1.51(1.18, 1.93)	0.001	0.479	0.006	0.018	0.171	0.675	0.954
Allele								
Overall	1.11(1.05, 1.18)	0.001	1.000	0.002	0.007	0.075	0.451	0.892
Caucasian	1.10(1.02, 1.18)	0.015	1.000	0.023	0.066	0.436	0.886	0.987
Breast cancer	1.09(1.01, 1.17)	0.030	1.000	0.049	0.133	0.628	0.945	0.994
PB	1.10(1.02, 1.17)	0.010	1.000	0.007	0.022	0.196	0.711	0.961
PCR-RFLP	1.10(1.02, 1.19)	0.014	1.000	0.050	0.136	0.634	0.946	0.994
High quality (> 9)	1.19(1.07, 1.33)	0.001	1.000	0.006	0.019	0.177	0.685	0.956

The results in false-positive report probability analysis were in bold, if the prior probability <0.2. OR: odds ratio; CI: confidence interval; ^a *P* value for significant test; ^b Statistical power was calculated using the number of observations in the meta-analysis and the OR and *P* value in this table.

Table S5. Meta-analysis of associations between rs4646537 and rs3782130 polymorphisms and cancer risk

Variables	N	Dominant model	Recessive model	Homozygote model	Heterozygote model	Allele model
		OR(95%CI)/I ² %/P _Q	OR(95%CI)/I ² %/P _Q	OR(95%CI)/I ² %/P _Q	OR(95%CI)/I ² %/P _Q	OR(95%CI)/I ² %/P _Q
rs4646537						
Overall	3	0.92(0.76, 1.10)/0/0.675	0.77(0.55, 1.09)/0/0.615	0.76(0.53, 1.10)/0/0.610	0.78(0.54, 1.12)/0/0.695	0.91(0.79, 1.05)/0/0.591
Caucasian	2	0.91(0.75, 1.10)/0/0.419	0.77(0.54, 1.09)/0/0.353	0.76(0.52, 1.09)/0/0.351	0.78(0.54, 1.12)/0/0.424	0.90(0.78, 1.04)/0/0.357
African	1	1.04(0.52, 2.07)	1.17(0.10, 13.13)	1.18(0.10, 13.31)	1.14(0.10, 13.62)	1.04(0.56, 1.94)
Prostate cancer	3	0.92(0.76, 1.10)/0/0.675	0.77(0.55, 1.09)/0/0.615	0.76(0.53, 1.10)/0/0.610	0.78(0.54, 1.12)/0/0.695	0.91(0.79, 1.05)/0/0.591
PCR-RFLP	2	0.95(0.78, 1.16)/0/0.793	0.79(0.56, 1.13)/0/0.752	0.79(0.55, 1.14)/0/0.743	0.80(0.56, 1.15)/0/0.776	0.93(0.80, 1.08)/0/0.710
SNPlex assay	1	0.77(0.49, 1.20)	0.19(0.01, 3.86)	0.18(0.01, 3.80)	0.23(0.01, 4.85)	0.74(0.48, 1.15)
High quality (> 9)	2	0.91(0.75, 1.10)/0/0.419	0.77(0.54, 1.09)/0/0.353	0.76(0.52, 1.09)/0/0.351	0.78(0.54, 1.12)/0/0.424	0.90(0.78, 1.04)/0/0.357
Low quality (≤ 9)	1	1.04(0.52, 2.07)	1.17(0.10, 13.13)	1.18(0.10, 13.31)	1.14(0.10, 13.62)	1.04(0.56, 1.94)
rs3782130						
Overall	6	0.99(0.87, 1.11)/0/0.533	1.14(0.95, 1.38)/0/0.417	1.11(0.91, 1.35)/0/0.526	1.19(0.97, 1.44)/1.4/0.407	1.02(0.94, 1.12)/0/0.665
Caucasian	2	1.09(0.89, 1.33)/0/0.616	1.21(0.85, 1.73)/0/0.353	1.27(0.87, 1.84)/0/0.369	1.16(0.80, 1.69)/0/0.329	1.10(0.94, 1.29)/0/0.760
African	1	1.05(0.44, 2.52)	1.11(0.10, 12.46)	1.11(0.10, 12.56)	1.07(0.08, 13.65)	1.06(0.47, 2.34)
Asian	3	0.93(0.79, 1.10)/13/0.317	1.13(0.82, 1.55)/50/0.134	1.06(0.84, 1.33)/28/0.251	1.18(0.84, 1.67)/51/0.130	0.99(0.89, 1.11)/3/0.357
Prostate cancer	3	1.09(0.89, 1.33)/0/0.879	1.21(0.85, 1.72)/0/0.648	1.26(0.87, 1.83)/0/0.665	1.16(0.80, 1.68)/0/0.620	1.10(0.94, 1.28)/0/0.950
NSCLC	2	0.87(0.73, 1.04)/0/0.976	1.14(0.70, 1.85)/75/0.045	1.04(0.68, 1.57)/61/0.111	1.24(0.75, 2.05)/73/0.053	0.96(0.85, 1.09)/0/0.331
Colorectal cancer	1	1.14(0.84, 1.55)	1.12(0.68, 1.83)	1.18(0.70, 1.98)	1.04(0.62, 1.77)	1.11(0.88, 1.40)
PCR-RFLP	4	0.98(0.83, 1.17)/0/0.616	0.98(0.74, 1.28)/0/0.638	0.96(0.72, 1.29)/0/0.517	1.01(0.75, 1.36)/0/0.753	0.98(0.86, 1.13)/0/0.558
Other methods	2	0.99(0.77, 1.27)/57/0.128	1.32(0.96, 1.69)/0/0.395	1.26(0.96, 1.65)/0/0.864	1.35(0.94, 1.76)/42/0.189	1.06(0.94, 1.19)/0/0.443
High quality (> 9)	4	0.96(0.84, 1.09)/1/0.387	1.15(0.94, 1.40)/40/0.173	1.10(0.89, 1.36)/27/0.251	1.21(0.98, 1.50)/38/0.186	1.01(0.92, 1.11)/0/0.558
Low quality (≤ 9)	2	1.13(0.85, 1.51)/0/0.861	1.12(0.95, 1.38)/0/0.995	1.18(0.71, 1.95)/0/0.963	1.04(0.62, 1.75)/0/0.986	1.10(0.88, 1.38)/0/0.907

Abbreviation: OR: Odds ratio; CI: Confidence interval; P_Q: P value of the Q-test for heterogeneity test.

Supplementary Figures

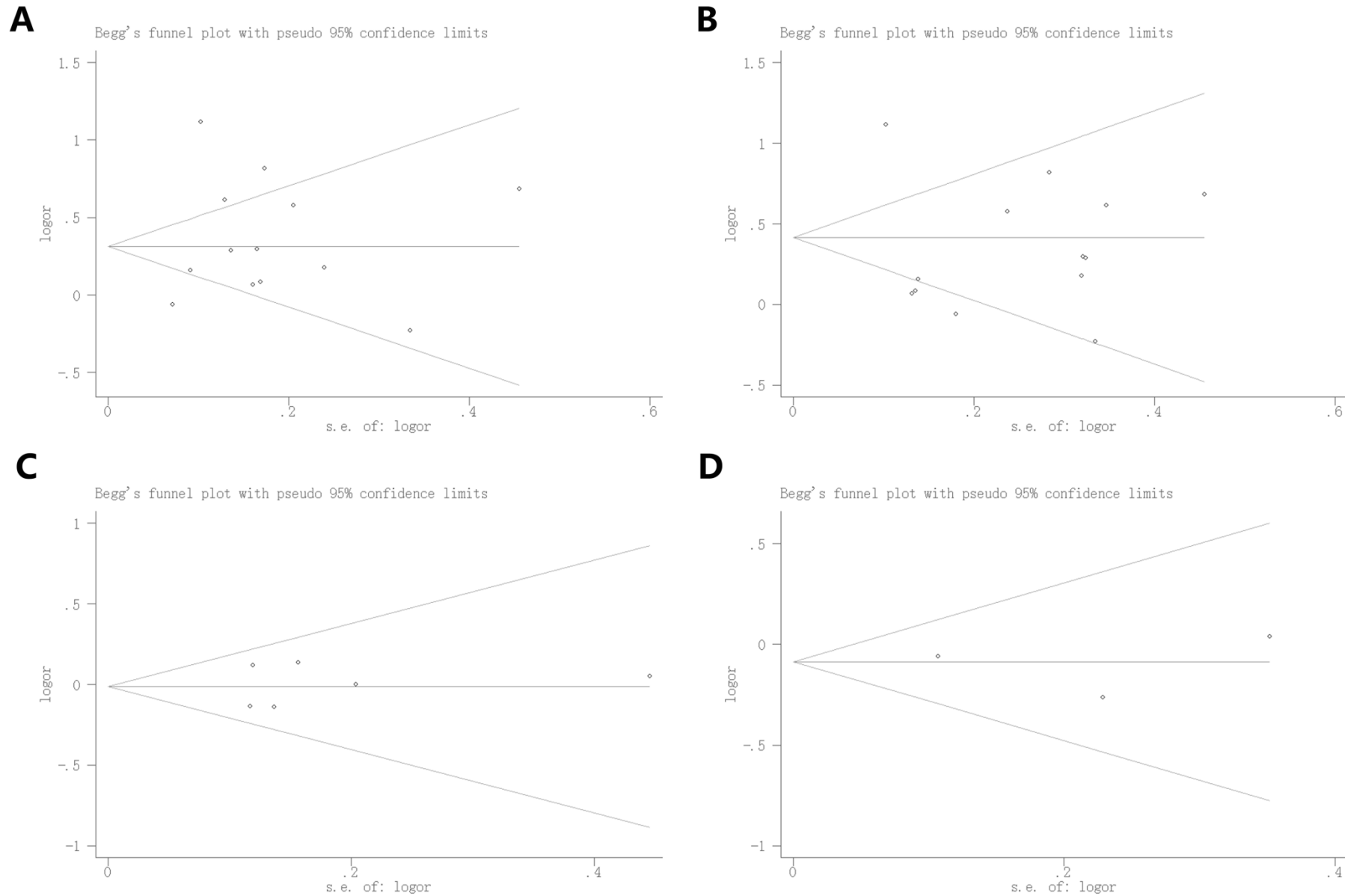


Figure S1. Begg's test for publication bias (dominant model). A rs4588; B rs7041; C rs3782130; D rs4646537

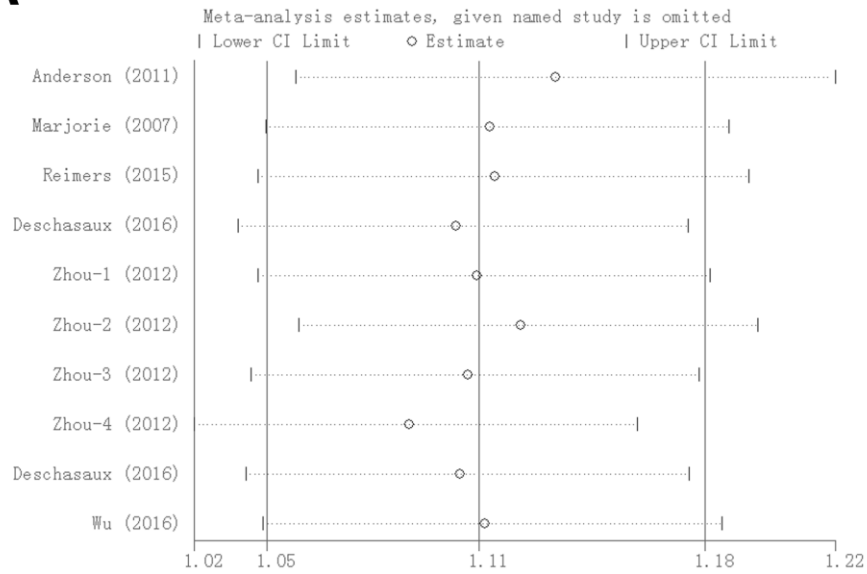
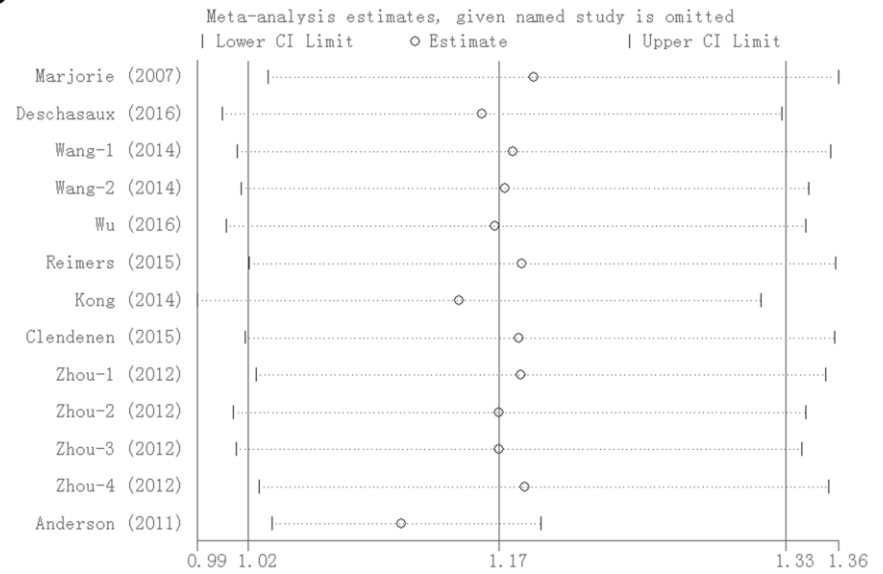
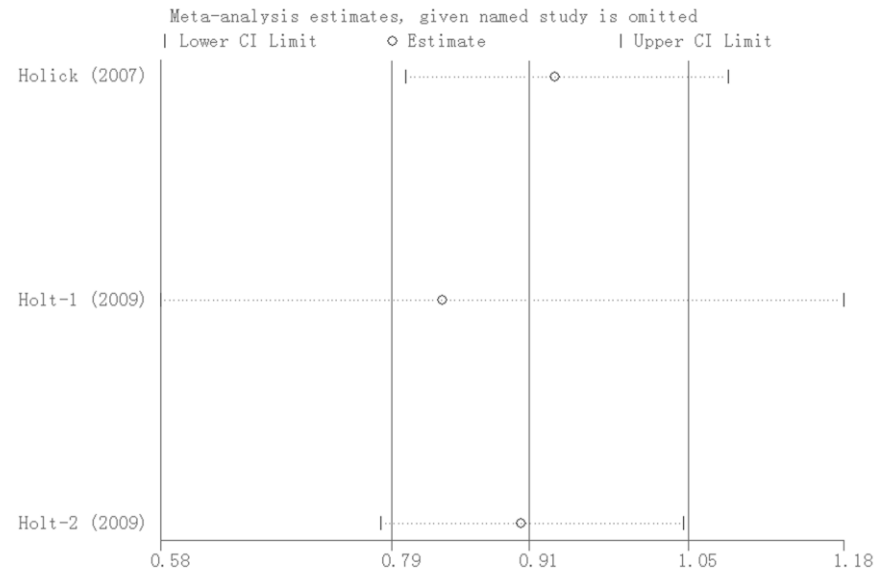
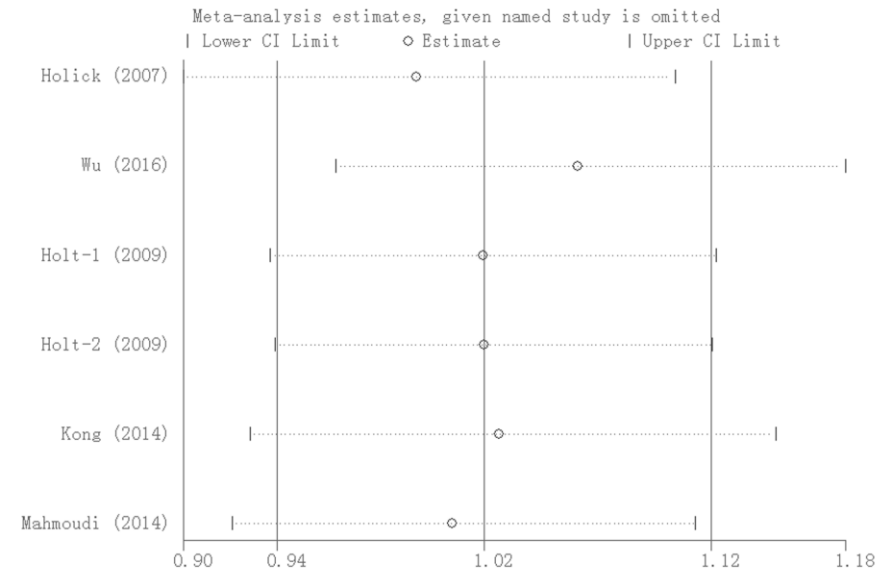
A**B****C****D**

Figure S2. Sensitivity analyses of the studies (allele model). A rs4588; B rs7041; C rs4646537; D rs3782130